

S5 Alignment. The X and ARF1 ORFs have a potential AUG start codon in all erythro- and tetraparvoviruses, respectively

Codon-based nucleotide alignment of the region surrounding the start of the X ORF of erythroparvoviruses (panel A) and of the ARF1 ORF of tetraparvoviruses (panel B). These alignments are derived from the reference alignment of the VP1 protein using TranslatorX. Numbering corresponds to the VP1 CDS.

Putative AUG start codons are highlighted in yellow. For each species, the putative AUG start codon is conserved in all isolates (not shown in this alignment). Note how the AUGs tend to be in a similar location within erythroparvoviruses (except in chipmunk parvovirus and seal parvovirus), and within tetraparvoviruses.

UAG or **UGA**: stop codon

AUG: putative start codon of the X ORF

A. Erythroparvoviruses

Parvovirus B19	185	UAG UUGCUCGCAUUAAAAUAACCUUAAAAAUUCCAGACUUAUAUAGUCAUUAUUCAAAGUC AUG GACAGUUAUCUGACCACCCCAU-----GCCUUAUCAUCCAGUAGCAGUCAUG	301
Simian parvovirus	293	ACCUUAAA---CAACAUUUACAAGACUAUAUAGACAAUCCAGAUAAAGUACACUU UAG ACUUGUCUC AUG GACCUCUCCAGAUUUCAGAGAA-----ACUGAGGCAGAACACAAAUCCUUUA	406
Rhesus macaque	299	AUCUACAA---AAACAAUUGAAAAACUAUAAAAUAAUCCAAACAAAUUAUACAUUACAGUUGUCUC AUG GACCUCUCCUGAUUUCAGAGAG-----UCUGAGGCACAAACAUAAUCCUCUA	412
Pigtailed macaque	194	UGGUUAAU---CGCAUUAAAAAAAU UAA AGACAAUCCUGAUUUUACACUGACUCCUUAAGUC AUG GCGCUCUCCAGAUUUCGAGAA-----UCUAAGGCUGAGCAUGAGAAGUCUA	307
Chipmunk parvovirus	311	CCGUAGCU---AACACAGCCAAGCGGU UAA AAACUGACGAGGAUCCCUA-----UCCUUUGGGGCCCCC UAA CAGAAAACGCCCCGGUUCGGUUGCGGAGCCAG AUG UGGCAAUUGUUU	427
Seal parvovirus	338	GGAGGCACUAUGGAUCCUAAAGGAGCAGGGCGCAGCACCCCCCGCUGAUCCAGACAUA UAG CAGGCCCUCCUCACAUACAGGGCCG-----GUGUUGGGGAGC AUG UCCCUAUCA	454

B. Tetraparvoviruses

Human parvovirus 4	467	UUUUUGAA---GACUCGC UAA CGAACUUUGCCAAAGAAGACU UAG ACACCUGGCAACAACUCCACGAGCAGUUUAUCAAACUCUUUACCCU-----CCAG AUG UCGGAGUCCACCUUGUUA	580
Porcine hokovirus	464	UCUUUGAG---GAGAGUGUAUCUCCUUGGUCUGAGGAAGACAAAAAAUU UGA AAACAGAUUGAAGGGCAGUUCAGGAAAUUUCCAUCCACCCACAGAUACGGAGG AUG GAGCCGAUAGCUACG	586
Yak hokovirus	491	UUUUUCAG---GGCAUGUUAUCUCCAUCAAACCUGAAGAUAGACCUAU UAG ACACCAUACAGAAGCAGUUUGAGGAGUUUUUUUUAUCCUCCUA UAG UGGAAC AUG CUGGACCAGGCGACUACA	613
Deer tetraparvovirus	491	ACUUUGAU---GGCAUGUUGUACCUUAUCCAGUGGAACAACAUCCAAUUG UAG AGCAGAU UAA AGGCUCAGUUUU UAA AUAUUUUUUAUCCGCCACCUA UAG CUGGAG AUG GAGUCGGUGUGACG	613
Ovine hokovirus	491	UUUUCAAU---GGUAUGUUGACGCCGUUGAUUCCGACCAGCGACCGUGGUCGAGCAGAUUACCCAGCAGUUCU UAG ACAUCUUUACCCCCCACCAGUGCAUGGCC AUG GCGGAGGUGUCGACA	613
Rodent tetraparvo	467	ACUUUGAC---CAGUUCAUACCCCCGGUGGACCCCCGGGAGCCCGAGAUUC UAA AGCAGGCCUUCAGCGCAUGG UAG AAUAUUACCACCCCGCCCU---CAGG AUG GCGGACCUGUCUCCUCCCC	586
Eidolon parvovirus	458	UUUUUGAU---GAGUCUGUGCUGGGCAGCGUUAGCGGAGACCCCGAAAACUUUGCUUUUGUGAAGCAGGCAG UAG UUAGUGCUUUUCAUCCUGCA-----G AUG GAGGAGCCGCUACUGAACAGC	574
Opposum tetraparvo	440	UUUUUACU---GACUCUAUUAGUGCGGGUG UAG CUGGAACA---CCACUCUGGGGAGAUACUGCAGAAGCUCUCAUGUCGGCCCUU-----GCAGGGA AUG GAAGUAUCAGAGGGU	544